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LNVPGSSSHDTLCTSTCTGFPLSTRVPGAEECERAVIDFVAFQDISIKRLQRLQLQALEAPE
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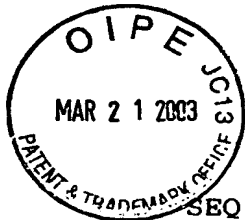
FIG. 1

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GCAGAGACAGGGGAGCGGCTGGTGTGCGCCAGTGCCCCCAGGCACCTTTGTGCAGCGG
CCGTGCCCGCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACGCAG
TTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCTCTGCGGGGAGCGTGAGGAG
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GCGCACGCTGGTTTTCTGCTTGAGACACGCATCGTGTCCACCTGGTGGCGGCGTGATTGCC
CCGGGCACCCCCAGCCAGAACACGCAGTGCCAGCCGTGCCCCCAGGCACCTTCTCAGCC
AGCAGCTCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCTGGCC
CTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCTGCACTGGCTTCCCC
CTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAGCGTGCCGTCATCGACTTTGTGGCT
TTCCAGGACATCTCCATCAAGAGGCTGCAGCGGCTGCTGCAGGCCCTCGAGGCCCCGGAG
GGCTGGGGTCCGACACCAAGGGCGGGCCGCGCGGCCCTTGAGCTGAAGCTGCGTCGGCGG
CTCACGGAGCTCCTGGGGGCGCAGGACGGGGCGCTGCTGGTGGCGGCTGCTGCAGGCGCTG
CGCGTGCCAGGATGCCCGGGCTGGAGCGGAGCGTCCGTGAGCGCTTCTCCTGTGCAC
TGATCCTGGCCCCCTCTTATTTATTCTACATCCTTGGCACCCTTGCCTGAAAGAGG
CTTTTTTTTAAATAAGAAGAAATGAGGTTTNTTAAAAAAAAAAAAAAAAAAAAA

FIG. 2

GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCTCTGNNG
GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCT
GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTTCTGCTTGAGAC
GCATCGTGTCCACCTGGTGGCGGCTGATTGCCCCGGGCACCCCCAGCCA
GAACACGCAGTGCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
CGTGCCGTCATCGACTTTGTGGCTTTCAGGACATCTCCAT

FIG. 3



SEQ ID NO: 4	128	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO: 5	1	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCNACTACACG
SEQ ID NO: 6	1	G
SEQ ID NO: 3	1	GCCGAGACAGCCCCACGACGTGTGGCCCGTGTCCACCGCGCCACTACACG
SEQ ID NO: 4	178	CA-TTCTGGAACCTACCTGGAGCGC
SEQ ID NO: 5	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
SEQ ID NO: 6	2	CAGTTCTGGAACCTACCTGGAGCGCTGCCGCTACTGCAACGTCCTCTGCGG
SEQ ID NO: 3	51	CAGTTCTGGAANTAACTGGAGCNCTGCCGCTACTGNAACGTCCTCTGNNG
SEQ ID NO: 5	101	GGAGCNTGAGGAGGAGGCANGNGCTTGCCACGCCACCCACAACCGCGCCT
SEQ ID NO: 6	52	GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
SEQ ID NO: 7	1	GAGGGGCCCCCAGGAGTGGTGGCCGGAGGTG
SEQ ID NO: 3	101	GGAGCGTGAGGAGGAGGCACGGGCTTGCCACGCCACCCACAACCGTGCCCT
SEQ ID NO: 5	151	GCNGCTGCAGCACCGGNTTCTTCGCGCACGCTGNNTTCTGCTTGAGCAC
SEQ ID NO: 6	102	GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGCAC
SEQ ID NO: 7	32	TGGCAGGGGTGAGTTGCTGGTCCCAGCCTTGACCCCTGAGCTAGGACAC
SEQ ID NO: 3	151	GCCGCTGCCGCACCGGCTTCTTCGCGCACGCTGGTTTCTGCTTGAGCAC
SEQ ID NO: 5	201	GCATCGTGTCCACCTGGTGNCGGCGTGATTGCNCCGGGCACCCCCAGCCA
SEQ ID NO: 6	152	GCATCGTGTCCACCTGGTGCCGGCGTGATTNCCCCGGGCACCCCCAGCCA
SEQ ID NO: 7	82	CAGTTCCCCTGACCTGTCTTCCCTCCTGGCTGCAGGCACCCCCAGCCA
SEQ ID NO: 8	1	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO: 10	1	CTTGTCCACCTGGTGCCGGCGTGATTNCCC-GGGCACCCCCAGCCA
SEQ ID NO: 3	201	GCATCGTGTCCACCTGGTGCCGGCGTGATTGCCCCGGGCACCCCCAGCCA
SEQ ID NO: 5	251	GAACACGCA-TGCAAAGCCGTG
SEQ ID NO: 7	132	GAACACGCAGN-CC-AGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 8	51	GAACACGCAG-GCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 10	47	GAACACGCAGTGCC-AGCCNT-CCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 9	1	AGCNGTGCNCCNCAGGCACCTTCTCAGCCAGCAGT
SEQ ID NO: 3	251	GAACACGCAGTGCCCTAGCCGTGCCCCCAGGCACCTTCTCAGCCAGCAGC
SEQ ID NO: 7	182	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 8	101	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 10	97	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCAACGCCCTGGNC-T
SEQ ID NO: 9	36	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 3	301	TCCAGCTCAGAGCAGTGCCAGCCCCACCGCAACTGCACGGCCCTGGGCCT
SEQ ID NO: 7	232	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAG
SEQ ID NO: 8	151	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 10	147	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 9	86	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACGCTGTGCACCAGCT
SEQ ID NO: 3	351	GGCCCTCAATGTGCCAGGCTCTTCTCCCATGACACCCTGTGCACCAGCT
SEQ ID NO: 10	197	GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 9	136	GCACTGGCTTCCCCCTCAGCACCAGGGTANAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 3	401	GCACTGGCTTCCCCCTCAGCACCAGGGTACCAGGAGCTGAGGAGTGTGAG
SEQ ID NO: 10	247	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 9	186	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT
SEQ ID NO: 3	451	CGTGCCGTCATCGACTTTGTGGCTTTCCAGGACATCTCCAT

FIG. 4

DNA30942
 1 MR A L E G P G L S L L C L V L A L P A L L P V P A V R G V A E T P T Y P W R D . A E T G
 1 M A P V A V W A A L A V G L E L W A A A H A L P A Q V A F T P V . A P E P G S T C R L R E Y Y D Q T
 htNFR2

	CRD 1										CRD 2																																			
DNA30942	C	A	Q	C	P	P	G	T	F	V	Q	R	P	C	R	R	D	S	P	T	C	G	P	C	P	P	P	R	H	Y	T	Q	F	W	N	Y	L	E	R	C	R	Y	C	N	V	L
50 A Q M C C	S	K	C	C	S	P	G	Q	H	A	K	V	F	C	T	K	T	S	D	T	V	C	D	S	C	E	D	S	T	Y	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R

	CRD 2										CRD 3																																								
DNA30942	C	G	E	R	E	E	A	R	A	C	H	A	T	H	N	R	A	C	R	C	R	T	G	F	F	.	.	A	H	A	G	.	.	F	C	L	E	H	A	S	C	P	P	G	A	G	V				
htNFR2	C	S	S	D	Q	Q	V	E	T	Q	A	C	T	R	E	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	G	C	R	L	C	A	P	L	R	K	C	R	P	G	F	G	V

	CRD 3										CRD 4																																						
DNA30942	139	I	A	P	G	T	P	S	Q	N	T	Q	C	Q	P	P	P	G	T	F	S	A	S	S	S	S	S	S	S	S																			
htNFR2	150	A	R	P	G	T	P	E	T	S	D	V	V	C	K	P	C	A	P	G	T	F	S	N	T	T	S	S	T	D	I	C	R	P	H	Q	I	C	N	V	V	A	. . .	I	P	G	N	A	S

	CRD 4																																																	
DNA30942	189 H	D	T	L	C	T	S	C	T	G	F	P	L	S	T	R	V	P	G	A	E	E	C	E	R	A	V	I	D	F	V	A	F	Q	D	I	S	I	K	R	L	Q	R	L	Q	A	L	E	A	
htNFR2	196 R	D	A	V	C	T	S	T	S	.	.	P	T	R	S	M	A	P	G	A	V	H	L	P	Q	P	V	S	T	R	S	Q	H	T	Q	P	T	P	E	P	S	T	A	P	S	T	S	F	L	L

DNA30942 239 P E G W G P T P . . R A G R A A L Q L K L R R R R L T E L L G A Q D G A L L V R L L Q A L R V A R M P
 244 P M G P S P A E G S T G D F A L P V G L I V G V T A L G L L I I G V V N C V I M T Q V K K P L .
 244 TNFR2

DNA30942 287 G L E R S V R E R F L P V H
 TNFR2 293 C L Q R E A K V P H L P A D K A R G T Q G P E Q Q H L L I T A P S S S L E S S A S A L D R R A

343 P T R N Q P Q A P G V E A S G A G E A R A S T G S S D S S P G G H G T Q V N V T C I V N V C S S S D
TTNFR2

393 H S S Q C S S Q A S S T M G D T D S S P S E S P K D E Q V P F S K E E C A F R S Q L E T P E T L L G
TTNR2

443 S T E E K P L P L G V P P D A G M K P S
TTFNR2

56F



DcR3 1 M R A L E G P G L S L C L V L A L P A L L P V P A V R G V A 31
OPG 1 M N K L L C C A L V F L D L S I K W T T Q E T F P - - - - - 25

DcR3 32 E T P T Y P W R R D A E T G E R L V C A Q C P P G T F V Q R P C 62
OPG 26 - - P K Y L H Y D E E T S H Q L L C D K C P P G T Y L K Q H C 54

DcR3 63 R R D S P T C G P C P P R R H Y T Q F W N Y L E R C R Y C N V 93
OPG 55 T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P 85

DcR3 94 L C G E R E E A R A C H A T H N R A C R C R T G F F A H A G 124
OPG 86 V C K E L Q Y V K Q E C N R T H N R V C E C K E G R Y L E I E 116

DcR3 125 F C L E H A S C P P G A G V I A P G T P S Q N T Q C Q P C P P 155
OPG 117 F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D 147

DcR3 156 G T F S A S S S E Q C Q P H R N C T A L G L A L N V P G S 186
OPG 148 G F F S N E T S S K A P C R K H T N C S V F G L L L T Q K G N 178

DcR3 187 S S H D T L C T S C T G F P L S T R V P G A E E C E R A V I D 217
OPG 179 A T H D N I C S G N S E S T Q K C G I D - V T L C E E A F F R 208

DcR3 218 F V A F Q D I S I K R L Q R L L Q A L E A P E G W G P T - P R 247
OPG 209 F A V P T K F T P N W L S V L V D N L P G T K V N A E S V E R 239

DcR3 248 A G R A A L Q L K L R R R L T E L L G A Q D G A L - L V R L L 277
OPG 240 I K R Q H S S Q E Q T F Q L L K L W K H Q N K A Q D I V K K I 270

DcR3 278 Q A L R V A R M P G L E R S V R E R F L P V H 300
OPG 271 I Q D I D L C E N S V Q R H I G H A N L T F E 293...

FIG. 6

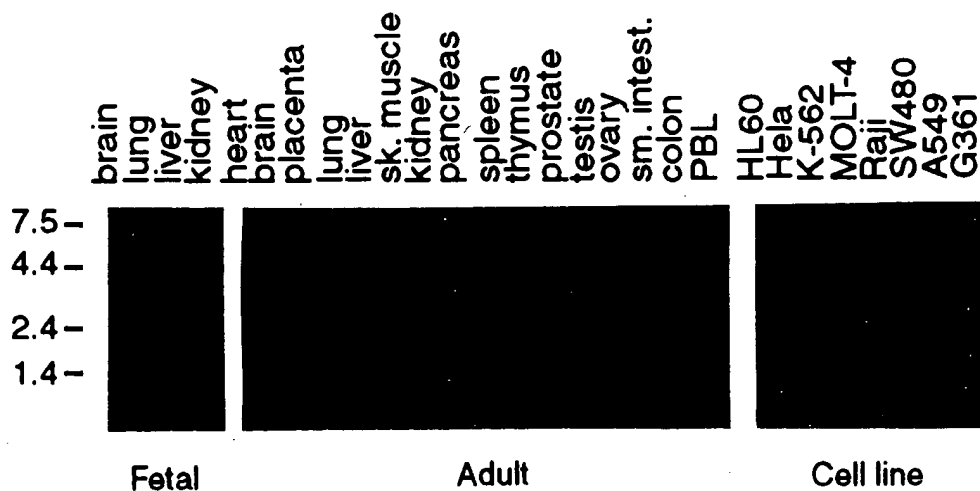
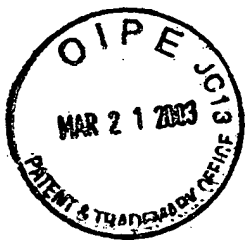


FIG. 7

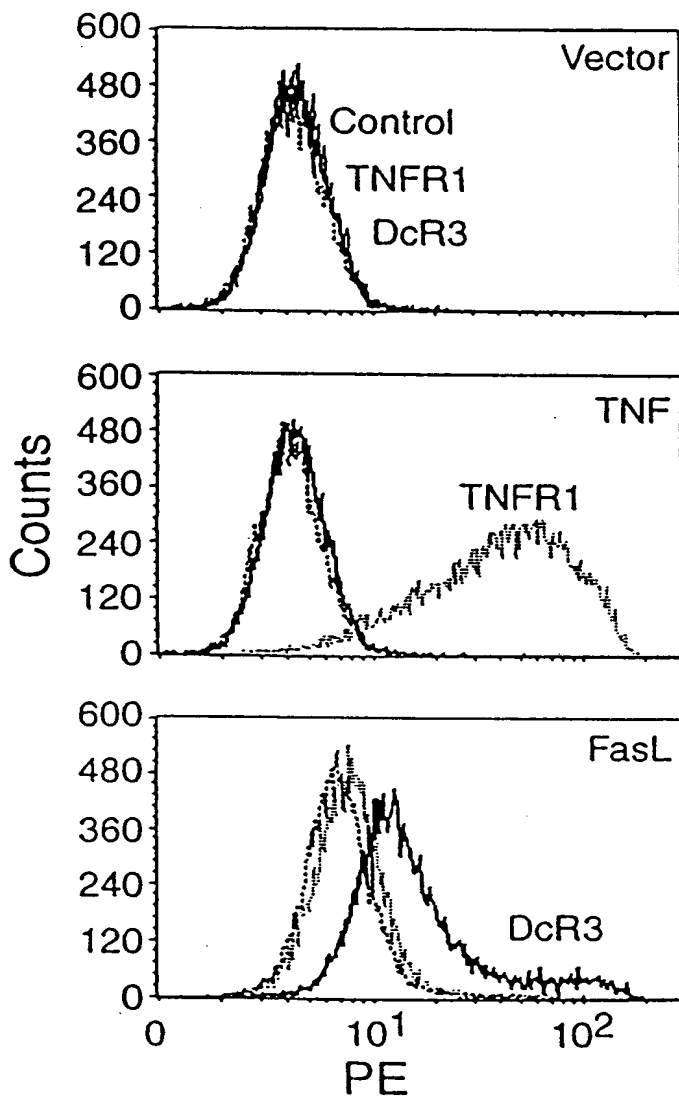


FIG. 8A

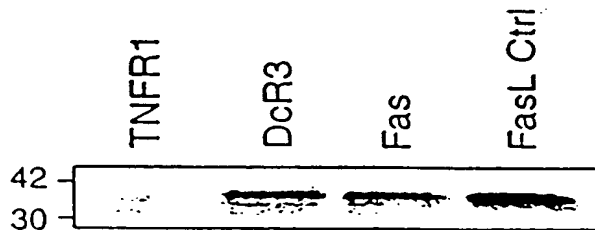


FIG. 8B

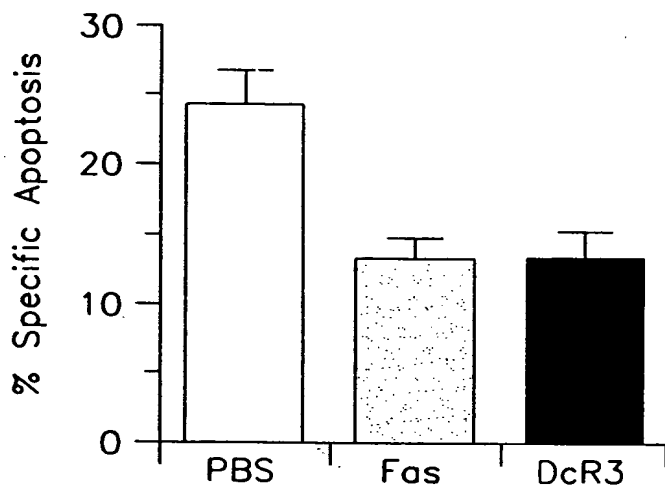


FIG. 9A

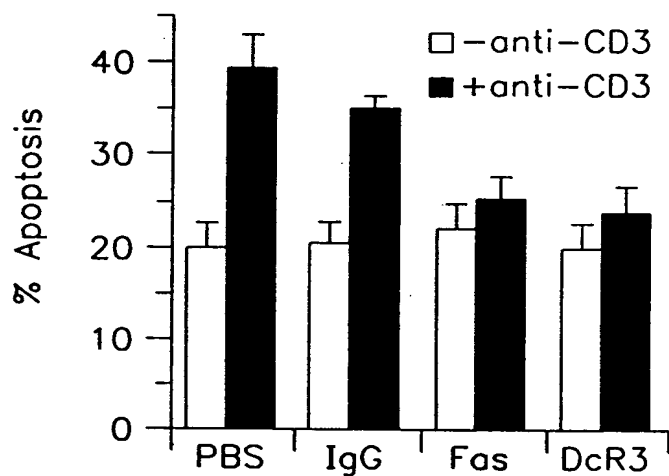


FIG. 9B

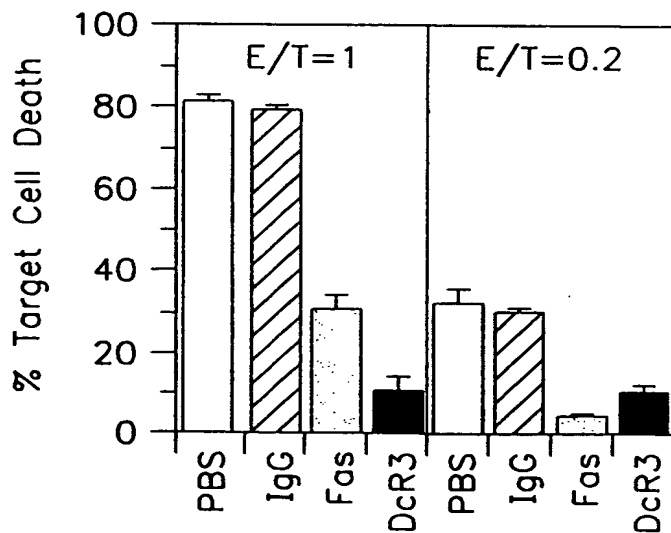


FIG. 9C

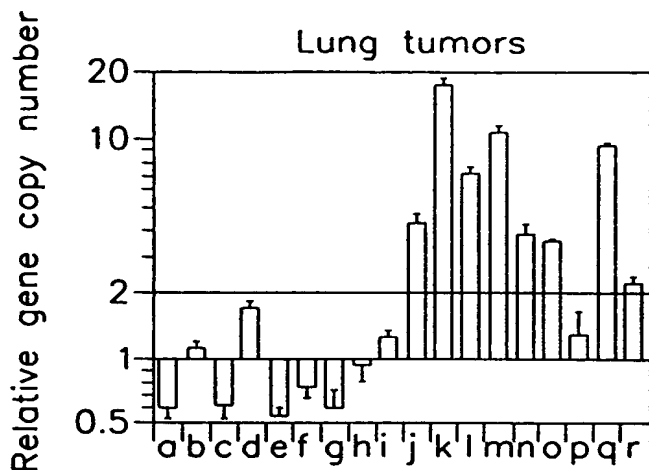
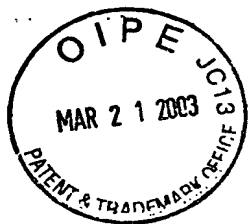


FIG. IOA

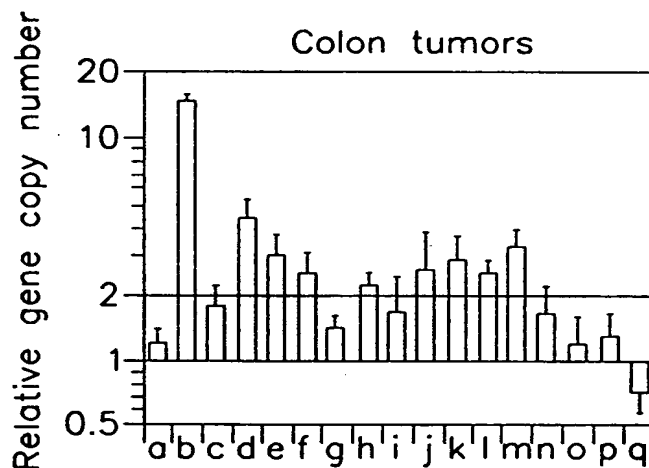


FIG. IOB

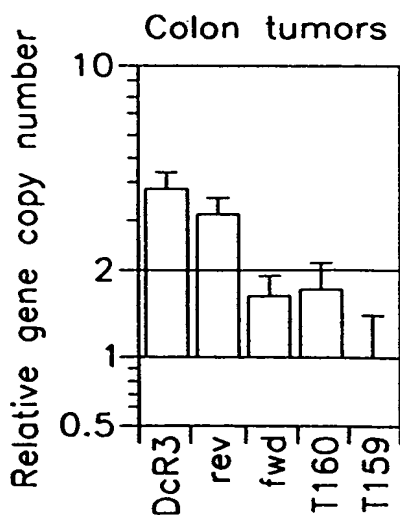


FIG. IOC

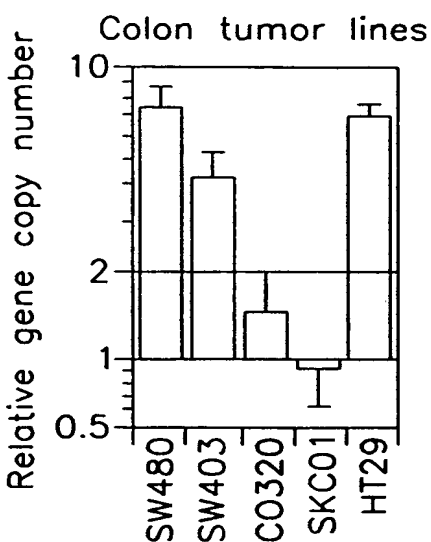


FIG. IOD

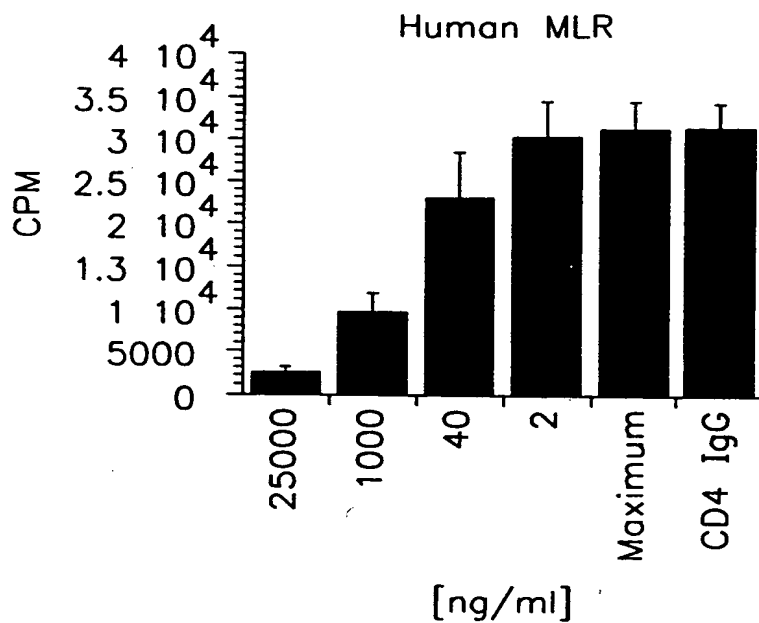
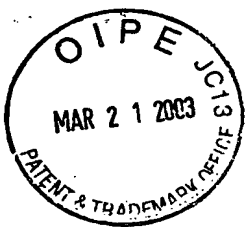


FIG. 1 IA

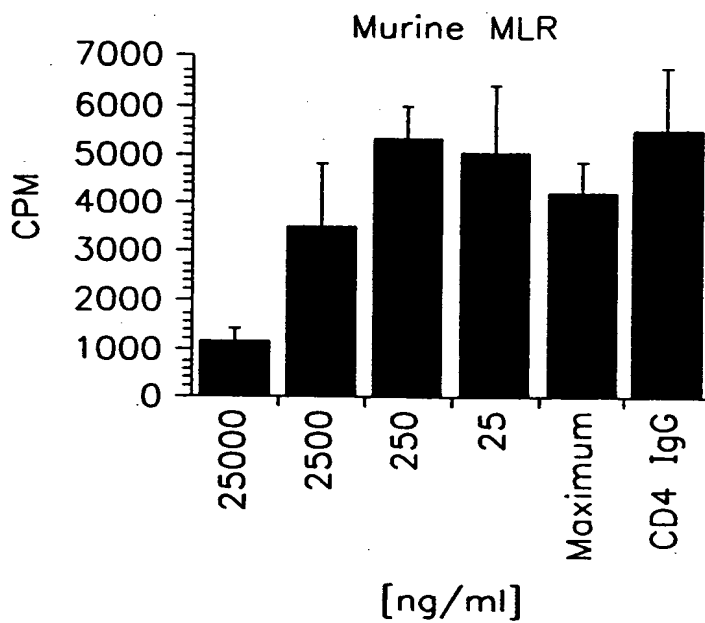


FIG. 1 IB

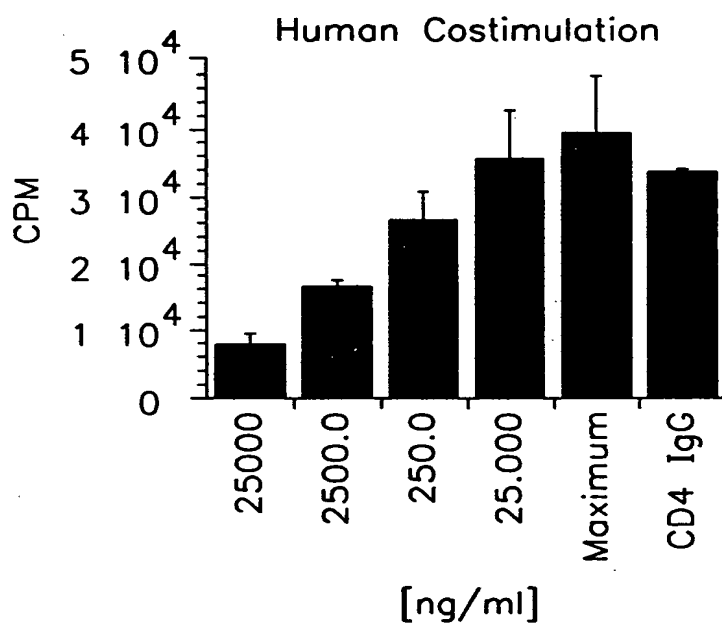
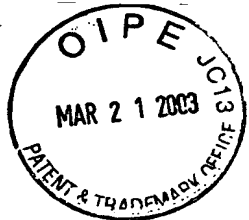


FIG. 1 IC



mAb	Isotype	Antigen Specificity (ELISA)				% Blocking (ELISA)
		DcR3	DR4	DR5	DcR1 OPG	
4B7.1.1	IgG1	+++	-	-	-	+
4C4.1.4	IgG2a	+++	-	-	-	-
5C4.14.7	IgG2b	+++	-	-	-	++
8D3.1.5	IgG1	+++	-	-	-	+/-
11C5.2.8	IgG1	+++	-	-	-	++

Antigen specificity was determined using 10 microgram/ml mAb.
% blocking activity was determined by ELISA at 100 fold excess of mAb to Fas ligand.

FIG. 12

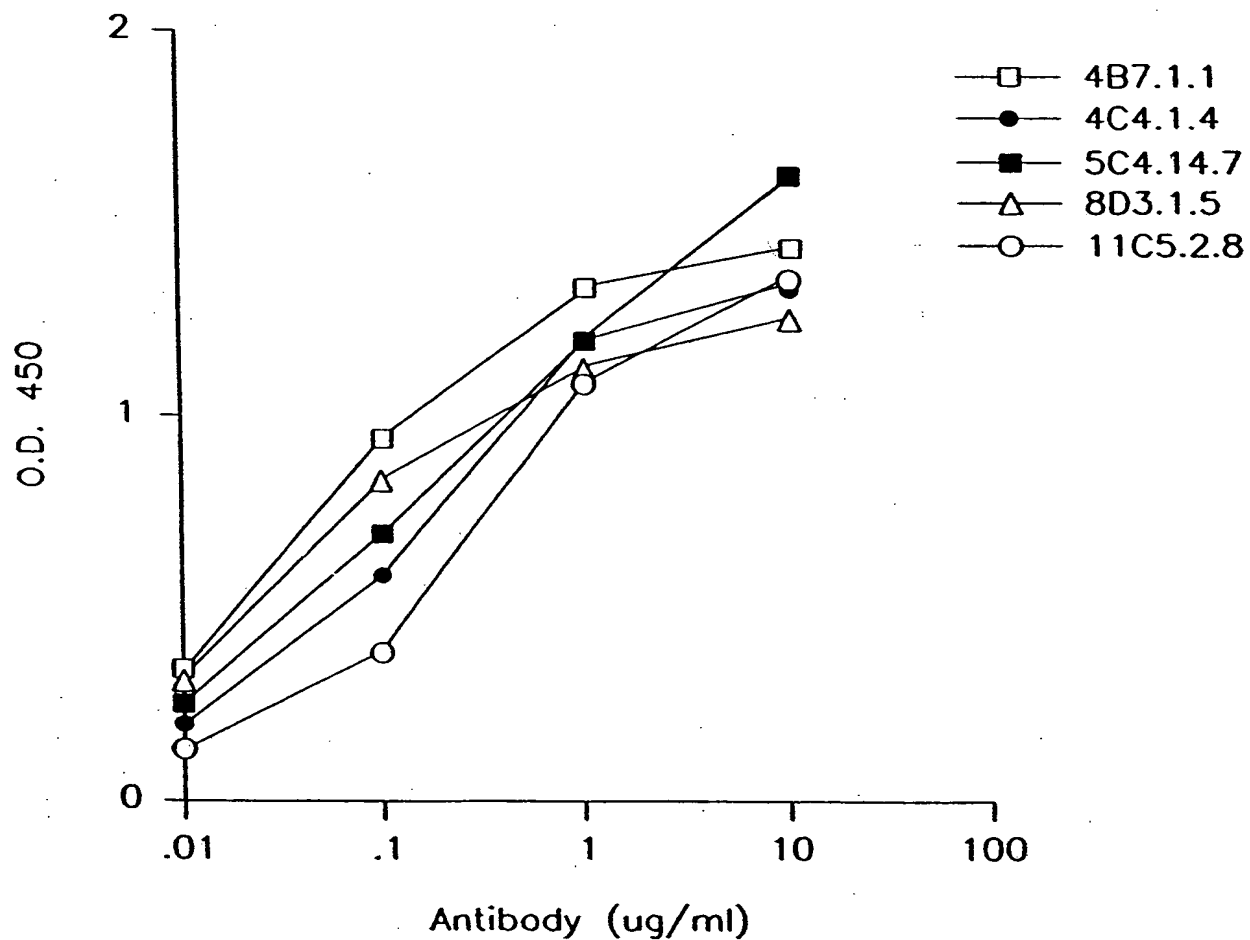


FIG. 13

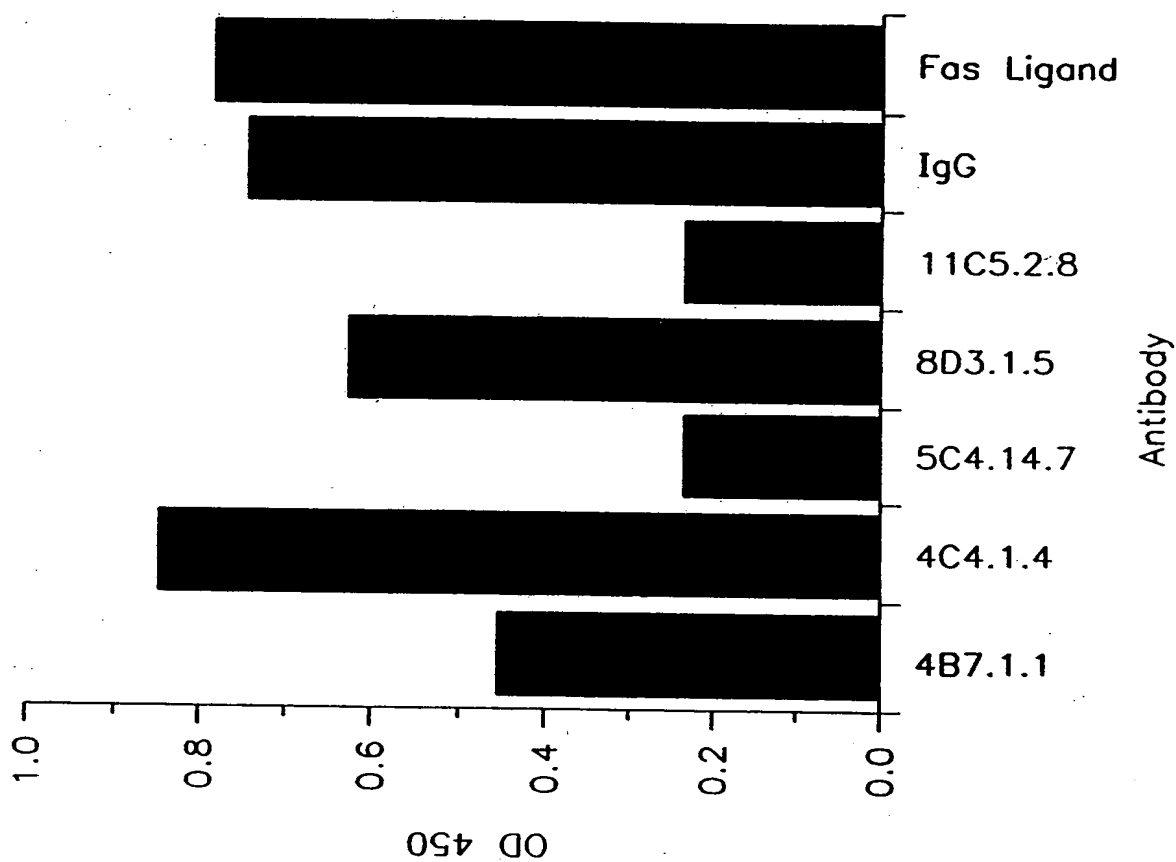


FIG. 14